

SEQUENCE LISTING

<110> LEUNG, SHAWN SHUI-ON

<120> REDUCING IMMUNOGENICITIES OF IMMUNOGLOBULINS BY
FRAMEWORK-PATCHING

<130> SBL-001US

<140> 09/892,613

<141> 2001-06-27

<160> 71

<170> PatentIn version 3.3

<210> 1

<211> 369

<212> DNA

<213> Artificial Sequence

<220>

<223> FR-patched heavy chain variable region sequence (Full DNA
Sequence) formed by joining the N- and C- terminal (SEQ 3 and 6)
halves at the KpeI site.

<220>

<221> V_region

<222> (1)..(369)

<400> 1

gaagtgcagc tgctggagtc tgggggaggc ttagtgcagc ctggagggtc cctgaggctc	60
tcctgtgcag cctctggatt ctccttcagt atctatgaca tgtcttgggt tcgccaggca	120
ccgggaaagg ggctggagtg ggtcgcatat attagtagtg gtggtggtac cacctactat	180
ccagacactg tgaagggccg attcaccatc tccagagaca atgccaagaa ctccctgtac	240
ctgcaaatga acagtctgag ggtggaggac acagccttat attactgtgc aagacatagt	300
ggctacggta gtagctacgg ggttttgttt gcttactggg gccaaaggac tctggtcact	360
gtctcttca	369

<210> 2
<211> 123
<212> PRT
<213> Chimaera sp.

<400> 2
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Ile Tyr
20 25 30

Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Tyr Ile Ser Ser Gly Gly Gly Thr Thr Tyr Tyr Pro Asp Thr Val
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Val Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Arg His Ser Gly Tyr Gly Ser Ser Tyr Gly Val Leu Phe Ala Tyr
100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 3
<211> 111
<212> DNA
<213> Artificial Sequence

<220>
<223> N-template is a synthetic sense-strand oligonucleotide encoding

amino acid 14-50 of the VH region (SEQ ID No. 2). The template is PCR-amplified by two primers (SEQ ID No. 4 and 5)

<220>

<221> V_region

<222> (1)..(111)

<400> 3

cctggagggt ccctgaggct ctctgtgca gcctctggat tctccttcag tatctatgac 60

atgtcttggg ttgccaggc accgggaaag gggctggagt gggtcgcata c 111

<210> 4

<211> 57

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' Primer is a synthetic sense-strand oligonucleotide encoding amino acid 1-19 of the VH region (SEQ ID No. 2). The 3' end of the primer overlaps with the 5' end of the template by 18 nucleotides.

<220>

<221> primer_bind

<222> (1)..(57)

<400> 4

gaagtgcagc tgctggagtc tgggggaggc ttagtgcagc ctggagggtc cctgagg 57

<210> 5

<211> 48

<212> DNA

<213> Artificial Sequence

<220>

<223> 3' Primer is a synthetic anti-sense-strand oligonucleotide encoding amino acid 43-59 of the VH region (SEQ ID No. 2). The primer overlaps with the template by 21 nucleotides.

<220>

<221> primer_bind

<222> (1)..(48)

<400> 5

gtaggtggta ccaccaccac tactaatgta tgcgaccac tccagccc

48

<210> 6

<211> 132

<212> DNA

<213> Artificial Sequence

<220>

<223> C-terminal is a synthetic sense-strand oligonucleotide encoding amino acid 68-111 of the VH region (SEQ ID No 2) The template is PCR-amplified by two primers (SEQ ID No 7 and 8)

<220>

<221> V_region

<222> (1)..(132)

<400> 6

ttcaccatct ccagagacaa tgccaagaac tcctgtacc tgcaaatgaa cagtctgagg 60

gtggaggaca cagccttata ttactgtgca agacatagtg gctacggtag tagctacggg 120

gttttgtttg ct 132

<210> 7

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' Primer is a synthetic sense-strand oligonucleotide encoding amino acid 55-74 of the VH region (SEQ ID No 2). The 3' end of the primer overlaps with the 5'end of the template by 21 nucleotides.

<220>

<221> primer_bind

<222> (1)..(60)

<400> 7
ggtggtacca cctactatcc agacactgtg aagggccgat tcaccatctc cagagacaat 60

<210> 8
<211> 57
<212> DNA
<213> Artificial Sequence

<220>
<223> 3' Primer is a synthetic anti-sense-strand oligonucleotide encoding amino acid 105-123 of the VH region (SEQ ID No 2). The primer and the template overlaps by 21 nucleotides.

<220>
<221> primer_bind
<222> (1)..(57)

<400> 8
tgaagagaca gtgaccagag tcccttggcc ccagtaagca aacaaaaccc cgtagct 57

<210> 9
<211> 321
<212> DNA
<213> Artificial Sequence

<220>
<223> FR-patched light chain variable region sequence formed by joining the N- and C- terminal (SEQ 11 and 14) halves at the KpeI site.

<220>
<221> V_region
<222> (1)..(321)

<400> 9
gatatccaga tgacccagtc tccatcctcc ctgtctgcct ctgtgggaga cagagtcacc 60

attagttgca gggcaagtca ggacattagc aattatttaa actggtatca gcagaaacca 120

ggtaaggctc cgaaactcct gatctactac actagtatat tacactcagg agtcccatca 180

aggttcagtg gcagtgggtc tggaacagaa ttactctca ccattagctc cctgcagcca 240

gaagattttg ccacttactt ttgccaacag ggtaatacgc ttccgtggac gttcgggtgga 300
 ggcaccaagg tggaaatcaa a 321

<210> 10
 <211> 107
 <212> PRT
 <213> Chimaera sp.

<400> 10
 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Asn Tyr
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35 40 45

Tyr Tyr Thr Ser Ile Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp
 85 90 95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
 100 105

<210> 11
 <211> 108
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> N-template is a synthetic sense-strand oligonucleotide encoding

amino acid 11-46 of the VL region (SEQ ID No. 10). The template is PCR-amplified by two primers (SEQ ID No. 12 and 13)

<220>

<221> V_region

<222> (1)..(108)

<400> 11

ctgtctgcct ctgtgggaga cagagtcacc attagttgca gggcaagtca ggacattagc 60

aattatttaa actggtatca gcagaaacca ggtaaggctc cgaaactc 108

<210> 12

<211> 51

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' Primer is a synthetic sense-strand oligonucleotide encoding amino acid 1-17 of the VH region (SEQ ID No 10). The 3' end of the primer overlaps with the 5'end of the template by 21 nucleotides.

<220>

<221> primer_bind

<222> (1)..(51)

<400> 12

gatatccaga tgacccagtc tccatcctcc ctgtctgcct ctgtgggaga c 51

<210> 13

<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> 3' Primer is a synthetic anti-sense-strand oligonucleotide encoding amino acid 40-53. The primer and the template overlaps by 18 nucleotides.

<220>

<221> primer_bind

<222> (1)..(40)

<400> 13

atatactagt gtagtagatc aggagtttcg gaggccttacc

40

<210> 14

<211> 120

<212> DNA

<213> Artificial Sequence

<220>

<223> C-terminal is a synthetic sense-strand oligonucleotide encoding amino acid 59-98 of the VH region (SEQ ID No 10) The template is PCR-amplified by tow primers (SEQ ID No 15 and 16)

<220>

<221> V_region

<222> (1)..(120)

<400> 14

ccatcaaggt tcagtggcag tgggtctgga acagaattta ctctcacat tagctccctg 60

cagccagaag attttgccac ttacttttgc caacagggta atacgcttcc gtggacgttc 120

<210> 15

<211> 49

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' Primer is a synthetic sense-strand oligonucleotide encoding amino acid 50-65 of the VH region (SEQ ID No. 10). The 3' end of the primer overlaps with the 5'end of the template by 21 nucleotides

<220>

<221> primer_bind

<222> (1)..(49)

<400> 15

ctacactagt atattacact caggagtccc atcaagggtc agtggcagt

49

<210> 16
<211> 48
<212> DNA
<213> Artificial Sequence

<220>
<223> 3' Primer is a synthetic anti-sense-strand oligonucleotide encoding amino acid 92-107 of the VH region (SEQ ID No 10). The primer and the template overlaps by 21 nucleotides.

<220>
<221> primer_bind
<222> (1)..(48)

<400> 16
tttgatttcc accttggtgc ctccaccgaa cgtccacgga agcgtatt 48

<210> 17
<211> 371
<212> DNA
<213> Artificial Sequence

<220>
<223> FR-patched heavy chain variable region sequence (Full DNA Sequence) formed by joining the N- and C- terminal (SEQ 19 and 22) halves at the KpeI site.

<220>
<221> V_region
<222> (1)..(371)

<400> 17
cagggtgcaac tgggtggcttc cggggctgag gtaaataagc ctggggcctc agtgaaggtc 60
tcctgcaagg cttctggcta cacatttacc agttacaata tgcactgggt acggcagcct 120
cctggaaggg gcctggaatg gattggagct atttatccag gaaatggatga tactagttac 180
aatcagaaat tcaagggcaa ggccacattg actgcagaca aatcctccag cacagcctac 240
atgcagctca gcagtctgac atctgaggac tctgcggtct attactgtgc aagatcgcac 300

tacggtagta actacgtaga ctactttgac tactggggcc aaggcaccac tgttacagtc 360

tcctctgata a 371

<210> 18

<211> 123

<212> PRT

<213> Chimaera sp.

<400> 18

Gln Val Gln Leu Val Ala Ser Gly Ala Glu Val Asn Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Asn Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp Ile
35 40 45

Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser His Tyr Gly Ser Asn Tyr Val Asp Tyr Phe Asp Tyr Trp
100 105 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser Asp
115 120

<210> 19

<211> 114

<212> DNA
<213> Artificial Sequence

<220>

<223> N-template is a synthetic sense-strand oligonucleotide encoding amino acid 12-49 of the VH region (SEQ ID No. 18). The template is PCR-amplified by two primers (SEQ ID No. 20 and 21)

<220>

<221> V_region
<222> (1)..(114)

<400> 19

aataagcctg gggcctcagt gaaggtctcc tgcaaggctt ctggctacac atttaccagt 60

tacaatatgc actgggtacg gcagcctcct ggaaggggcc tggaatggat tgga 114

<210> 20

<211> 57

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' Primer is a synthetic sense-strand oligonucleotide encoding amino acid 1-19 of the VH region (SEQ ID No 18). The 3' end of the primer overlaps with the 5'end of the template by 24 nucleotides.

<220>

<221> primer_bind
<222> (1)..(57)

<400> 20

caggtgcaac tggtaggcttc cggggctgag gtaaataagc ctggggcctc agtgaag 57

<210> 21

<211> 55

<212> DNA

<213> Artificial Sequence

<220>

<223> 3' Primer is a synthetic anti-sense-strand oligonucleotide

encoding amino acid 43-60 of the VH region (SEQ ID No 18). The primer and the template overlaps by 21 nucleotides.

<220>

<221> primer_bind

<222> (1)..(55)

<400> 21

tgtaactagt atcaccattt cctggataaa tagctccaat ccattccagg ccct 55

<210> 22

<211> 126

<212> DNA

<213> Artificial Sequence

<220>

<223> C-terminal is a synthetic sense-strand oligonucleotide encoding amino acid 70-111 of the VH region (SEQ ID No 18) The template is PCR-amplified by tow primers (SEQ ID No 23 and 24)

<220>

<221> V_region

<222> (1)..(126)

<400> 22

ttgactgcag acaaatcctc cagcacagcc tacatgcagc tcagcagtct gacatctgag 60

gactctgcgg tctattactg tgcaagatcg cactacggta gtaactacgt agactacttt 120

gactac 126

<210> 23

<211> 61

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' Primer is a synthetic sense-strand oligonucleotide encoding amino acid 57-76 of the VH region (SEQ ID No 18). The 3' end of the primer overlaps with the 5'end of the template by 21 nucleotides.

<220>

<221> primer_bind

<222> (1)..(61)

<400> 23

tgatactagt tacaatcaga aattcaaggg caaggccaca ttgactgcag acaaatcctc 60

c 61

<210> 24

<211> 59

<212> DNA

<213> Artificial Sequence

<220>

<223> 3' Primer is a synthetic anti-sense-strand oligonucleotide encoding amino acid 105-123 of the VH region (SEQ ID No 18). The primer and the template overlaps by 21 nucleotides.

<220>

<221> primer_bind

<222> (1)..(59)

<400> 24

tgatcagagg agactgtaac agtggtgcct tggccccagt agtcaaagta gtctacgta 59

<210> 25

<211> 321

<212> DNA

<213> Artificial Sequence

<220>

<223> FR-patched light chain variable region sequence (Full DNA Sequence) formed by joining the N- and C- terminal (SEQ 27 and 30) halves at the BspEI site.

<220>

<221> V_region

<222> (1)..(321)

<400> 25

gatattcaac tcacacagtc tccatcaagt ctttctgcat ctgtggggga cagagtcaca	60
attacttgca gggccagctc aagtttaagt ttcatgcact ggtaccagca gaagccagga	120
tcctccccc aaccctggat ttatgccaca tccaacctgg cttccggagt ccctagtcgc	180
ttcagtggca gtgggtctgg gaccgagttc actctcaca tcagcagttt gcagcctgaa	240
gatttcgcc cttatttctg ccatcagtgg agtagtaacc cgctcacgtt cgggtgctggg	300
accaagctga ccgttctacg g	321

<210> 26

<211> 107

<212> PRT

<213> Chimaera sp.

<400> 26

Asp	Ile	Gln	Leu	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly
1				5				10						15	

Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Ser	Ser	Leu	Ser	Phe	Met
		20					25					30			

His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Ser	Ser	Pro	Lys	Pro	Trp	Ile	Tyr
	35					40					45				

Ala	Thr	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser
	50				55						60				

Gly	Ser	Gly	Thr	Glu	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu
65				70					75					80	

Asp	Phe	Ala	Thr	Tyr	Phe	Cys	His	Gln	Trp	Ser	Ser	Asn	Pro	Leu	Thr
			85						90					95	

Phe	Gly	Ala	Gly	Thr	Lys	Leu	Thr	Val	Leu	Arg
		100					105			

<210> 27
<211> 129
<212> DNA
<213> Artificial Sequence

<220>
<223> N-template is a synthetic sense-strand oligonucleotide encoding amino acid 9-51 of the VL region (SEQ ID No. 26). The template is PCR-amplified by two primers (SEQ ID No. 28 and 29)

<220>
<221> V_region
<222> (1)..(129)

<400> 27
tcaagtcttt ctgcatctgt gggggacaga gtcacaatta cttgcagggc cagctcaagt 60
ttaagtttca tgcactggta ccagcagaag ccaggatcct cccccaacc ctggatttat 120
gccacatcc 129

<210> 28
<211> 45
<212> DNA
<213> Artificial Sequence

<220>
<223> 5' Primer is a synthetic sense-strand oligonucleotide encoding amino acid 1-15 of the VH region (SEQ ID No 26). The 3' end of the primer overlaps with the 5'end of the template by 21 nucleotides.

<220>
<221> primer_bind
<222> (1)..(45)

<400> 28
gatattcaac tcacacagtc tccatcaagt ctttctgcat ctgtg 45

<210> 29
<211> 40

<212> DNA

<213> Artificial Sequence

<220>

<223> 3' Primer is a synthetic anti-sense-strand oligonucleotide encoding amino acid 45-57. The primer and the template overlaps by 21 nucleotides.

<220>

<221> primer_bind

<222> (1)..(40)

<400> 29

ggactccgga agccagggtg gatgtggcat aaatccaggg

40

<210> 30

<211> 120

<212> DNA

<213> Artificial Sequence

<220>

<223> C-terminal is a synthetic sense-strand oligonucleotide encoding amino acid 61-100 of the VH region (SEQ ID No 26) The template is PCR-amplified by tow primers (SEQ ID No 31 and 32)

<220>

<221> V_region

<222> (1)..(120)

<400> 30

ttcagtggca gtgggtctgg gaccgagttc actctcaca tcagcagttt gcagcctgaa 60

gatttcgcca cttatttctg ccatcagtgg agtagtaacc cgctcacgtt cggtgctggg 120

<210> 31

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' Primer is a synthetic sense-strand oligonucleotide encoding amino acid 54-67 of the VH region (SEQ ID No 18). The 3' end of

the primer overlaps with the 5'end of the template by 21 nucleotides.

<220>

<221> primer_bind

<222> (1)..(43)

<400> 31

ggcttccgga gtcctagtc gcttcagtgg cagtgggtct ggg

43

<210> 32

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> 3' Primer is a synthetic anti-sense-strand oligonucleotide encoding amino acid 94-107 of the VH region (SEQ ID No 26). The primer and the template overlaps by 21 nucleotides.

<220>

<221> primer_bind

<222> (1)..(42)

<400> 32

ccgtagaacg gtcagcttgg tcccagcacc gaacgtgagc gg

42

<210> 33

<211> 123

<212> PRT

<213> Mus sp.

<400> 33

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Ala Phe Ser Ile Tyr
20 25 30

Asp Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val

35

40

45

Ala Tyr Ile Ser Ser Gly Gly Gly Thr Thr Tyr Tyr Pro Asp Thr Val
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
 65 70 75 80

Leu Gln Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Tyr Tyr Cys
 85 90 95

Ala Arg His Ser Gly Tyr Gly Ser Ser Tyr Gly Val Leu Phe Ala Tyr
 100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala
 115 120

<210> 34

<211> 107

<212> PRT

<213> Mus sp.

<400> 34

Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
 1 5 10 15

Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Asn Tyr
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
 35 40 45

Tyr Tyr Thr Ser Ile Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln

80

95

105

<213> Homo sapiens

15

30

45

60

80

95

110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala

115

120

<210> 36
<211> 29
<212> PRT
<213> Homo sapiens

<400> 36
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Pro Gly Gly Ser
1 5 10 15

Leu Arg Leu Ser Cys Ala Thr Thr Gly Phe Ala Phe Ser
20 25

<210> 37
<211> 30
<212> PRT
<213> Homo sapiens

<400> 37
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser
20 25 30

<210> 38
<211> 30
<212> PRT
<213> Homo sapiens

<400> 38
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser
20 25 30

<210> 39

<211> 14
<212> PRT
<213> Homo sapiens

<400> 39
Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ala
1 5 10

<210> 40
<211> 32
<212> PRT
<213> Homo sapiens

<400> 40
Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr Leu Gln
1 5 10 15

Met Asn Ser Leu Arg Val Glu Asp Thr Ala Leu Tyr Tyr Cys Ala Arg
20 25 30

<210> 41
<211> 11
<212> PRT
<213> Homo sapiens

<400> 41
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Thr
1 5 10

<210> 42
<211> 107
<212> PRT
<213> Homo sapiens

<400> 42
Asp Ile Gln Met Thr Gln Thr Thr Ser Ser Leu Ser Ala Ser Leu Gly
1 5 10 15

Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu Ile
35 40 45

Tyr Tyr Thr Ser Ile Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln
65 70 75 80

Glu Asp Phe Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp
85 90 95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
100 105

<210> 43

<211> 23

<212> PRT

<213> Homo sapiens

<400> 43

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Ser Cys
20

<210> 44

<211> 15

<212> PRT

<213> Homo sapiens

<400> 44

Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Tyr
1 5 10 15

<210> 45

<211> 32
<212> PRT
<213> Homo sapiens

<400> 45
Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
1 5 10 15

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Phe Cys
20 25 30

<210> 46
<211> 10
<212> PRT
<213> Homo sapiens

<400> 46
Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
1 5 10

<210> 47
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 47
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ser Phe Ser Ile Tyr
20 25 30

Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Tyr Ile Ser Ser Gly Gly Gly Thr Thr Tyr Tyr Pro Asp Thr Val

50

55

60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Tyr
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Val Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Arg His Ser Gly Tyr Gly Ser Ser Tyr Gly Val Leu Phe Ala Tyr
100 105 110

Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
115 120

<210> 48

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic polypeptide

<400> 48

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Asp Ile Ser Asn Tyr
20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
35 40 45

Tyr Tyr Thr Ser Ile Leu His Ser Gly Val Pro Ser Arg Phe Ser Gly
50 55 60

Ser Gly Ser Gly Thr Glu Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

80

95

105

<213> Mus sp.

15

30

45

60

80

95

110

Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Asp

115

120

<210> 50
 <211> 107
 <212> PRT
 <213> Mus sp.

<400> 50
 Gln Ile Val Leu Ser Gln Ser Pro Ala Ile Leu Ser Ala Ser Pro Gly
 1 5 10 15

Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Leu Ser Phe Met
 20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr
 35 40 45

Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
 50 55 60

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Val Glu Ala Glu
 65 70 75 80

Asp Ala Ala Thr Tyr Phe Cys His Gln Trp Ser Ser Asn Pro Leu Thr
 85 90 95

Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg
 100 105

<210> 51
 <211> 123
 <212> PRT
 <213> Homo sapiens

<400> 51
 Gln Val Gln Leu Arg Gln Pro Gly Ala Glu Leu Val Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Asn Met His Trp Val Lys Gln Thr Pro Gly Gln Gly Leu Glu Trp Ile
35 40 45

Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys
85 90 95

Ala Arg Ser His Tyr Gly Ser Asn Tyr Val Asp Tyr Phe Asp Tyr Trp
100 105 110

Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Asp
115 120

<210> 52

<211> 30

<212> PRT

<213> Homo sapiens

<400> 52

Gln Val Gln Leu Val Ala Ser Gly Ala Glu Val Asn Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr
20 25 30

<210> 53

<211> 14

<212> PRT

<213> Homo sapiens

<400> 53

Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp Ile Gly
1 5 10

<210> 54

<211> 32

<212> PRT

<213> Homo sapiens

<400> 54

Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr Met Glu
1 5 10 15

Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Arg
20 25 30

<210> 55

<211> 32

<212> PRT

<213> Homo sapiens

<400> 55

Arg Ala Thr Ile Ser Val Asp Thr Ser Lys Asn Gln Phe Ser Leu Asn
1 5 10 15

Leu Ser Ser Val Thr Ala Ala Asp Thr Ala Val Tyr Cys Cys Ala Arg
20 25 30

<210> 56

<211> 11

<212> PRT

<213> Homo sapiens

<400> 56

Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser
1 5 10

<210> 57

<211> 107

<212> PRT

<213> Homo sapiens

<400> 57

Gln Ile Val Leu Ser Gln Ser Pro Ala Ile Leu Ser Ala Ser Pro Gly
1 5 10 15

Glu Lys Val Thr Met Thr Cys Arg Ala Ser Ser Ser Leu Ser Phe Met
20 25 30

His Trp Tyr Gln Gln Lys Pro Gly Ser Ser Pro Lys Pro Trp Ile Tyr
35 40 45

Ala Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
50 55 60

Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Val Glu Ala Glu
65 70 75 80

Asp Ala Ala Thr Tyr Phe Cys His Gln Trp Ser Ser Asn Pro Leu Thr
85 90 95

Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg
100 105

<210> 58

<211> 23

<212> PRT

<213> Homo sapiens

<400> 58

Asp Ile Gln Leu Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
1 5 10 15

Asp Arg Val Thr Ile Thr Cys
20

<210> 59
<211> 22
<212> PRT
<213> Homo sapiens

<400> 59
Asn Leu Met Leu Ile Gln Pro Pro Ser Val Ser Glu Ser Pro Gly Lys
1 5 10 15

Thr Val Thr Met Thr Cys
20

<210> 60
<211> 15
<212> PRT
<213> Homo sapiens

<400> 60
Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Pro Val Ile Tyr
1 5 10 15

<210> 61
<211> 32
<212> PRT
<213> Homo sapiens

<400> 61
Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Glu Phe Thr
1 5 10 15

Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Phe Cys
20 25 30

<210> 62
<211> 32
<212> PRT
<213> Homo sapiens

<400> 62
Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr

1 5 10 15

Leu Thr Ile Thr Ser Leu Gln Pro Glu Asp Phe Ala Ala Tyr Phe Cys
20 25 30

<210> 63

<211> 32

<212> PRT

<213> Homo sapiens

<400> 63

Gly Val Pro Ser Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Phe
1 5 10 15

Leu Thr Ile Ser Ser Leu Arg Pro Glu Asp Val Ala Thr Tyr Phe Cys
20 25 30

<210> 64

<211> 32

<212> PRT

<213> Homo sapiens

<400> 64

Gly Val Pro Ala Arg Phe Ser Gly Tyr Asn Ser Gly Asn Ser Ala Phe
1 5 10 15

Leu Thr Ile Asn Arg Val Glu Ala Gly Asp Glu Ala Asp Tyr Phe Cys
20 25 30

<210> 65

<211> 11

<212> PRT

<213> Homo sapiens

<400> 65

Phe Gly Gly Gly Thr Lys Val Glu Ile Lys Arg
1 5 10

<210> 66

<211> 11
<212> PRT
<213> Homo sapiens

<400> 66
Phe Gly Val Gly Ser Lys Val Glu Ser Lys Arg
1 5 10

<210> 67
<211> 11
<212> PRT
<213> Homo sapiens

<400> 67
Phe Gly Ala Gly Thr Lys Leu Thr Val Leu Arg
1 5 10

<210> 68
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 68
Gln Val Gln Leu Val Ala Ser Gly Ala Glu Val Asn Lys Pro Gly Ala
1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
20 25 30

Asn Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp Ile
35 40 45

Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
50 55 60

Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr

65					70						75				80
Met	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Tyr	Cys
				85					90					95	

Ala	Arg	Ser	His	Tyr	Gly	Ser	Asn	Tyr	Val	Asp	Tyr	Phe	Asp	Tyr	Trp
			100				105						110		

Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser
	115						120		

<210> 69
 <211> 107
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic polypeptide

<400> 69															
Asp	Ile	Gln	Leu	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly
1				5				10						15	

Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Ser	Ser	Leu	Ser	Phe	Met
			20					25					30		

His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Ser	Ser	Pro	Lys	Pro	Trp	Ile	Tyr
		35					40					45			

Ala	Thr	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser
	50					55					60				

Gly	Ser	Gly	Thr	Glu	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu
65					70					75					80

Asp	Phe	Ala	Thr	Tyr	Phe	Cys	His	Gln	Trp	Ser	Ser	Asn	Pro	Leu	Thr
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

85

90

95

Phe Gly Ala Gly Thr Lys Leu Thr Val Leu Arg
 100 105

<210> 70

<211> 122

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 polypeptide

<400> 70

Gln Val Gln Leu Val Ala Ser Gly Ala Glu Val Asn Lys Pro Gly Ala
 1 5 10 15

Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
 20 25 30

Asn Met His Trp Val Arg Gln Pro Pro Gly Arg Gly Leu Glu Trp Ile
 35 40 45

Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn Gln Lys Phe
 50 55 60

Lys Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser Thr Ala Tyr
 65 70 75 80

Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr Cys
 85 90 95

Ala Arg Ser His Tyr Gly Ser Asn Tyr Val Asp Tyr Phe Asp Tyr Trp
 100 105 110

Gly Gln Gly Thr Thr Val Thr Val Ser Ser

115

120

<210> 71

<211> 107

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
polypeptide

<400> 71

Asp	Ile	Gln	Leu	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly
1				5				10						15	

Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Ser	Ser	Leu	Ser	Phe	Met
			20					25					30		

His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Val	Pro	Val	Ile	Tyr
		35					40					45			

Ala	Thr	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser
	50					55					60				

Gly	Ser	Gly	Thr	Glu	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu
65					70					75					80

Asp	Phe	Ala	Thr	Tyr	Phe	Cys	His	Gln	Trp	Ser	Ser	Asn	Pro	Leu	Thr
				85					90					95	

Phe	Gly	Ala	Gly	Thr	Lys	Leu	Thr	Val	Leu	Arg
			100					105		